

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:09:30 ; Search time 8498.8 Seconds
(without alignments)
32.874 Million cell updates/sec

Title: US-09-851-670-18

Perfect score: 26
Sequence: 1 ttatgtgacatcttgcacgat 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 111874

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estopl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hnc:*
10: gb_est1:*
11: gb_est2:*
12: gb_hnc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rnd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	57.7	59	10	AL593945
2	14.8	56.9	52	10	BE322167
3	14.6	56.2	52	13	A2647203
4	14.4	55.4	46	13	AQ025201
5	14.4	55.4	46	13	AQ025201
6	14	53.8	52	10	AA935402
7	13.8	53.1	29	10	AA250048
8	13.6	52.3	59	11	T61794
9	13.4	51.5	31	10	A1973656
10	13.4	51.5	33	13	A2760071
11	13.4	51.5	46	10	AA232414
12	13.4	51.5	55	10	AA288258

c 13	13.4	51.5	55	10	AA566958
c 14	13.4	51.5	60	10	BE317966
c 15	13.2	50.8	44	10	AW355214
c 16	13.2	50.8	44	13	A2778327
c 17	13.2	50.8	52	11	H28465
c 18	13.2	50.8	55	11	T70039
c 19	13.2	50.8	58	10	A1959431
c 20	13	50.0	23	13	TA266D020
c 21	13	50.0	55	10	AA754857
c 22	13	50.0	56	11	BE638275
c 23	13	50.0	60	11	H55533
c 24	12.8	49.2	42	11	D67715
c 25	12.8	49.2	43	11	A1085127
c 26	12.8	49.2	43	11	WA1103
c 27	12.8	49.2	50	10	AA999944
c 28	12.8	49.2	51	13	BH011434
c 29	12.8	49.2	55	10	AA142590
c 30	12.8	49.2	55	13	A2775247
c 31	12.8	49.2	57	13	A2454242
c 32	12.8	49.2	58	10	AA792062
c 33	12.8	49.2	58	10	A1707554
c 34	12.8	49.2	58	10	A1707742
c 35	12.8	49.2	58	11	N92878
c 36	12.8	49.2	59	13	A2813936
c 37	12.8	49.2	60	11	B1082549
c 38	12.6	48.5	23	13	A2316806
c 39	12.6	48.5	27	13	A2838052
c 40	12.6	48.5	38	11	D18219
c 41	12.6	48.5	40	10	A1140952
c 42	12.6	48.5	50	10	AU104339
c 43	12.6	48.5	50	10	AU104340
c 44	12.6	48.5	50	10	AU104344
c 45	12.6	48.5	50	10	AU104352

ALIGNMENTS

RESULT 1	AL593945	59 bp	mrna	EST	30-JUL-2001
LOCUS	AL593945				
DEFINITION	AL593945 XGC-gastrula silurana tropicallis cDNA clone Tga004c16 5', mRNA sequence.				
ACCESSION	AL593945.1	GI:15006006			
VERSION	AL593945				
KEYWORDS	EST.				
SOURCE	Western clawed frog.				
ORGANISM	Silurana tropicalis				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Silurana.				
AUTHORS	Huckle, E., Taylor, R., McMurray, A., Ashurst, J.L., Zorn, A.M. and Rogers, J.				
TITLE	Xenopus tropicalis EST project 2001				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Huckle E Sanger Centre Hinxton, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk Sanger Xenopus tropicalis EST project 2001 TROPCALIS_SEQUENCE_ID: Tga004c16.sp6 Sequencing primer: SP6 This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.				
FEATURES	Location/Qualifiers				
source	1..59				
	/organism="Silurana tropicalis"				
	/db_xref="taxon:8364"				
	/clone="Tga004c16"				
	/clone_lib="XGC-gastrula"				
	/dev_stage="gastrula (stages 10.5-13 mixed)"				
	/lab_host="Escherichia coli DH10B"				

```

BASE COUNT
ORIGIN
18 a      11 c      16 g      14 t
/Note=Vector: PCS107; Site.1: EcoRI; Site.2: NotI; cDNA
was oligo dT primed from 5ug of Poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into PCS107 with EcoRI at the 5' end and NotI at the 3'
end."

```

Query Match	57.7%	Score 15;	DB 10;	Length 59;
Best Local Similarity	78.3%;	Pred. No. 2.6e+04;		
Matches 18; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0

```
Qy 1 ttaattgtggccatcttgtccag 23
    ||| | | ||||| |||
Db 28 TTAGTCTTGCCATCTTTACCAg 6
```

RESULT	2
BE322167	
LOCUS	BE322167 52 bp mRNA EST 21-DEC-2000
DEFINITION	NF010G05I1E1037 Insect herbivory Medicago truncatula cDNA clone
ACCESSION	NF010G05I1E1037 mRNA sequence.
VERSION	BE322167
KEYWORDS	BE322167.2 GI:11964189
SOURCE	EST.
ORGANISM	barrel medic. Medicago truncatula

REFERENCE	1 (bases 1 to 52)
AUTHORS	Korth, K.J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores
TITLE	, H.R., Imman, J.T., Weller, J.W. and May, G.D.
JOURNAL	Expressed Sequence Tags from the Samuel Roberts Noble Foundation
COMMENT	Medicago truncatula insect herbivory library (unpublished 2000) On Jul. 14, 2000, this sequence version replaced gi:9195944.

217 Plant Science Building, Fayetteville, AR 72701, USA
Tel.: 501 575 5191
Fax: 501 575 7601
Email: khorth@comp.uark.edu
Medicago Genome Initiative accession: MGI:S:23992
Insert Length: 659 Std Error: 0.00
Plate: 010 row: G column: 05
Seq primer: TCACACAGGAACACCTTGAC.

FEATURES	SOURCE
location/Qualifiers	1. 52
/organism="Medicago truncatula"	
/db_xref="taxon:3880"	
/clone="NF010505IN"	
/clone_lib="Insect herbivory"	
/tissue_type="local and systemic leaves"	
/dev_stage="mature"	
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic undamaged leaves from injured plants) and wounded leaves were harvested and pooled."	
	11 a 17 c 3 g 21 t

Query Match	56.9%;	Score 14.8;	DB 10;	Length 52;
Best Local Similarity	73.1%;	Pred. No. 3.1e+04;		

QY 1 ttatgtgcacatccttgtccagcat 26
|| || | ||||| | |||||

Db 23 TTCTTCTCTTCATCTTTCTCAAGCAT 48

RESULT 3

LOCUS	AZ647203	52 bp	DNA	GSS	14-DEC-2000
DEFINITION	IM0513004R Mouse 10kb plasmid UUGC1M library. Mus musculus genomic clone UUGC1M0513004 R, DNA sequence.				

VERSION	A2647203.1	GI:11778434
KEYWORDS	GSS.	
SOURCE	house mouse.	

REFERENCE	1 (bases 1 to 52)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Loncaric, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
 84112, USA
 Tel.: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0513 row: 0 column: 04
 Seq primer: CACACAGAAACACTTATGCAC
 Class: plasmid ends
 High quality sequence stop: 52.

FEATURES	Location/Qualifiers
source	1. .52

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0513004"
/clone_1lb="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMW42 (g14732114[gb|AF12972.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

BASE COUNT	21 a	13 c	8 g	10 t
ORIGIN				

Query Match	Score	DB	Length
Best Local Similarity	73.1%	Pred. No. 3.1e+04	
Query Match	56.9%	DB 10	Length 52
Query Match	56.2%	DB 13	Length 52

Matches	17;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
1	ttatctgtgacatctttgtcc	21							

Db 33 TTATGTGGTGCTCCTTGACC 13

RESULT 4

LOCUS A0025201 46 bp DNA GSS 23-AUG-2000

DEFINITION EP(3)1219 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, DNA sequence.

ACCESSION A0025201

VERSION A0025201.1 GI:3265553

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster
fruit fly.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

TITLE

Insertion site preferences of the P transposable element in Drosophila melanogaster

JOURNAL

MEDLINE

COMMENT

Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P element

The P element insertion position is base 39 in the 46 bases. This insertion position refers to the first base of the 8 base target recognition sequence.

Class: transposon-tagged.

FEATURES

SOURCE

Location/Qualifiers

1..46

/db_xref="taxon:7227"

/clone_lib="Drosophila melanogaster EP line"

/note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains a single EP transposable element insertion. (The generation of these insertion strains is described in Roth P, Szabo K, Bailey A, Laverly T, Rehm J, Rubin GM, Weigmann K, Milan K, Benes V, Ansong W, Cohen SM, 1998. Systematic gain-of-function genetics in Drosophila. Development 6:1049-1057.) The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfly.berkeley.edu/P-distrupt/Inverse_pcr.html."

BASE COUNT

ORIGIN

9 a

14 c

11 g

12 t

Query Match 55.4%; Score 14.4; DB 13; Length 46;
Best Local Similarity 75.0%; Pred. No. 4.5e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY

1 ttatgtgcatcttgcagc 24

Db

18 TTACTTGGCGCTTCTTGACGAC 41

RESULT 5

LOCUS

DEFINITION A1920251 55 bp mRNA EST 29-JUL-1999

1761 Pine Lambda Zap Xylem Library Pinus taeda cDNA clone

95-PL21NC5U, mRNA sequence.

ACCESSION

A1920251

VERSION A1920251.1 GI:5649883

KEYWORDS

SOURCE

ORGANISM

loblolly pine.
Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 55)
Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R.
The Pine Gene Discovery Project
Unpublished (1999)

JOURNAL

COMMENT

Contact: Ross Whetten
Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh, NC, 27695-8008
Tel: 919-515-7800
Fax: 919-515-7801
Email: rosswhetten@unc.edu
Seq primer: M13 Forward.

FEATURES

SOURCE

Location/Qualifiers

1..55

/organism="Pinus taeda"

/db_xref="taxon:3352"

/clone="95-PL21NC5U"

/note="Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI; Differentiating xylem was collected from the main stem of a 35-year old loblolly pine tree harvested during the growing season. RNA isolation and library preparation followed the methods of Allona et al., PNAS 95:9693-8, 1998"

BASE COUNT 13 a 12 c 15 g 13 t 2 others

ORIGIN

Query Match 55.4%; Score 14.4; DB 10; Length 55;
Best Local Similarity 72.0%; Pred. No. 4.5e+04;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY

1 ttatgtgcatcttgcagc 25

Db

46 TGTAGAGGCGCTCATTTGCCAGCA 22

RESULT 6

LOCUS

DEFINITION

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

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AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

AA935402/c

Trace considered overall poor quality
Seq primer: 40m13 fwd. ET from Amerisham
High quality sequence stop: 1.

FEATURES

source

1. .52

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1459637"

/clone_lib="NCI-CGAP_K1d6"

/sex="mixed"

/tissue_type="Kidney tumor"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: kidney; Vector: Bluescript SK-; Site_1:

ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:

GAAATCGGACGAG 3' 3' adaptor sequence: 5'

CTCGAGTTTTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."

BASE COUNT 19 a 8 c 11 g 14 t

ORIGIN

Query Match 53.8%; Score 14; DB 10; Length 52;

Best Local Similarity 77.3%; Pred. No. 6.6e+04;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 tttgtggcattctgtccagcat 26

Db 50 TATGACTATCTTGTTCATTAT 29

RESULT 7

AM250048 29 bp mRNA EST 07-JAN-2000

LOCUS 2819281.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819281 3',

ACCESSION mRNA sequence.

VERSION AM250048.1 GI:6593041

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 29)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2819281.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapds-remail.nih.gov

Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing

project clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LNL at:

www.bio.lnln.gov/dbp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector

Trimming: cross-match from University of Washington Genome Center

PHRAP suite. Poly-T identification: Patmatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 9 contiguous

PHRED high quality bases following vector sequence. Very low

Quality Sequence: Trace file contained 29 contiguous distinct peaks

following vector sequence. Polyadenylation: Based upon the presence

of a XhoI site followed by a run of 14 or more T residues at the

beginning of the sequence, this CDNA insert was polyadenylated.

Plate: L1CML row: D column: 2

High quality sequence stop: 9.

Location/Qualifiers

1. .29

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2819281"

/clone_lib="NIH_MGC-7"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:

ECORI; CDNA made by oligo-dT priming. Directionally

cloned into EORI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 3 a. 6 c 2 g 18 t

ORIGIN

Query Match 53.1%; Score 13.8; DB 10; Length 29;

Best Local Similarity 72.0%; Pred. No. 7.7e+04;

Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 ttattgtggcattctgtccagca 25

Db 4 TTTTGTGCTTCTTTTCCACCA 28

RESULT 8

T61794 59 bp mRNA EST 14-FEB-1995

LOCUS yb05e08.s1 Stratagene liver (#937224) Homo sapiens cDNA clone

IMAGE:78950 3' similar to gb:K02403 COMPLEMENT C4 PRECURSOR (HUMAN

); mRNA sequence.

VERSION T61794.1 GI:665037

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 59)

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapell, B.,

Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins

, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore

, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,

Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevas, E.,

Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (3), 807-828 (1996)

97044478

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1721

High quality sequence starts: 1 High quality sequence stops: 1

Source: IMAGE Consortium, LNL This clone is available royalty-free

for further information. Trace considered overall poor quality

Insert Length: 1721 Std Error: 0.00

Seq primer: -21m13

High quality sequence stop: 1.

Location/Qualifiers

1. .59

/organism="Homo sapiens"

/db_xref="GDB:498695"

/db_xref="taxon:9606"

/clone="IMAGE:78950"

/clone_lib="Stratagene Liver (#937224)"

/sex="male"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

/note="Organ: liver; Vector: pBluescript SK, Site_1: EORI

Site 2: XhoI: Cloned unidirectionally. Primer: Oligo-dT. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb. Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTAATGCGATTTTTTTTTTTTTT 3' "

BASE COUNT	11 a	20 c	16 g	11 t	1 others
ORIGIN					

Query Match	52.3%	Score 13.6	DB 11	Length 59
Best Local Similarity	76.2%	Pred. No. 9.6e+04		
Matches 16	Conservative 0	Mismatches 5	Indels 0	Gaps 0

```

QY      5  tgtggccatcttgtccagca 25
          ||| | ||| | ||| |||
Db     31  TGTAGNCATCCTCGTCCTGCA 51

```

[illegible]

ACCESSION	AI973656	
VERSION	AI973656.1	GI:5770482

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

1 (bases 1 to 31)
Shoemaker, R., Keim, P., Vockin, L., Erpelting, J., Corvelli, V., Khanna
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers
Y., Person, B., Waller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
R., Ralter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M.,
R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R./Public Soybean EST Project.
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 266 1800
Fax: 314 266 1810
Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Cairway Circle St. Louis, Missouri 63114 For further information
call: (800) 430-0030 or (314) 427-3322 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Trace considered overall poor quality
Seq. primer: -40RP from Gdbco
High quality sequence step: 1.

FEATURES
Source

```

/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl020-1054"
/clone_lib="Gm-cl020"
/tissue_type="root nodules of greenhouse grown plants"
/lab_host="XL10-G010"
/notes="Vector: plusscript II SK+; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from nodules on the roots of 2.5 month-old Glycine max
'Williams' plants that were greenhouse grown. The cDNA
library was prepared using the Stratagene plusscript II
SK(+) library construction kit. First strand synthesis was
performed with 5-methyl dctp, hence the ligated cDNA was
nonmethylated. A modification of Stratagene's

```

BASE COUNT
ORIGIN

query Match	51.5%;	Score 13.4;	DB 10;	Length 31;
Best Local Similarity	73.9%;	Pred. No. 1.1e+05;		
Matches 17;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;

```
QY      3 atgtgcatccttgtccagca 25
          |||||
Db      9 ATGTGCCCACTTATCAACA 31
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RESULT 10

LOCUS	AZ760071	33 bp	DNA	GSS	16-FEB-2001
DEFINITION	IM0553C03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0553C03 R, DNA sequence.				

ACCESSION	AZ760071
VERSION	AZ760071.1
	GI:12867513

ORGANISM

REFERENCE
1 (pages 1 to 33)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (pages 1 to 33)

AUTHORS

TITLE

JOURNAL
COMMENT

University of Utah
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FEATURES
SOURCE

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0553C03"
/clone_lib="mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, RI-resistant, F-"

```


Fax: 302-831-3411
Email: joan@udel.edu, www.chickest.udel.edu.
Location/Qualifiers

FEATURES
source

1. .44
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pnf-b.pk0001.a6"
/clone_lib="chicken fat cDNA library PBSII"
/sex="Male and Female"
/tissue_type="fat"
/lab_host="E.coli DH10B"
/note="Vector: PBSII"

BASE COUNT 21 a 6 c 3 g 14 t
ORIGIN

Query Match 50.8%; Score 13.2; DB 10; Length 44;
Best Local Similarity 69.2%; Pred. No. 1.4e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 ttatgtgacacatcttgcagcat 26
||||||| | ||| | |||||
DB 28 TTATTGTTAATTTTATTATACAGCAP 3

Search completed: March 9, 2002, 00:09:32
Job time: 11048 sec